

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Anderson, Darrell R.

70600 (ii) TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
(B) STREET: 699 Prince Street
(C) CITY: Alexandria
(D) STATE: VA
(E) COUNTRY: USA
(F) ZIP: 22314

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/487,550
(B) FILING DATE: 07-JUN-1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Teskin, Robin L.
(B) REGISTRATION NUMBER: 35,030
(C) REFERENCE/DOCKET NUMBER: 012712-131

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 703 836 6620
(B) TELEFAX: 703 836 2021

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..705

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG	AGG	GTC	CCC	GCT	CAG	CTC	CTG	GGG	CTC	CTG	CTG	CTC	TGG	CTC	CCA	48
Met	Arg	Val	Pro	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Pro	
1				5				10					15			
GGT	GCA	CGA	TGT	GCC	TAT	GAA	CTG	ACT	CAG	CCA	CCC	TCG	GTG	TCA	GTG	96
Gly	Ala	Arg	Cys	Ala	Tyr	Glu	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Val	
			20				25						30			
TCC	CCA	GGA	CAG	ACG	GCC	AGG	ATC	ACC	TGT	GGG	GGA	GAC	AAC	AGT	AGA	144
Ser	Pro	Gly	Gln	Thr	Ala	Arg	Ile	Thr	Cys	Gly	Gly	Asp	Asn	Ser	Arg	
		35					40					45				
AAT	GAA	TAT	GTC	CAC	TGG	TAC	CAG	CAG	AAG	CCA	GCG	CGG	GCC	CCT	ATA	192
Asn	Glu	Tyr	Val	His	Trp	Tyr	Gln	Gln	Lys	Pro	Ala	Arg	Ala	Pro	Ile	
	50					55				60						
CTG	GTC	ATC	TAT	GAT	GAT	AGT	GAC	CGG	CCC	TCA	GGG	ATC	CCT	GAG	CGA	240
Leu	Val	Ile	Tyr	Asp	Asp	Ser	Asp	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	
65				70				75						80		
TTC	TCT	GGC	TCC	AAA	TCA	GGG	AAC	ACC	GCC	ACC	CTG	ACC	ATC	AAC	GGG	288
Phe	Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Asn	Gly	
				85				90						95		
GTC	GAG	GCC	GGG	GAT	GAG	GCT	GAC	TAT	TAC	TGT	CAG	GTG	TGG	GAC	AGG	336
Val	Glu	Ala	Gly	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Arg	
			100				105					110				
GCT	AGT	GAT	CAT	CCG	GTC	TTC	GGA	GGA	GGG	ACC	CGG	GTG	ACC	GTC	CTA	384
Ala	Ser	Asp	His	Pro	Val	Phe	Gly	Gly	Gly	Thr	Arg	Val	Thr	Val	Leu	
		115					120					125				
GGT	CAG	CCC	AAG	GCT	GCC	CCC	TCG	GTC	ACT	CTG	TTC	CCG	CCC	TCC	TCT	432
Gly	Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	
	130					135					140					
GAG	GAG	CTT	CAA	GCC	AAC	AAG	GCC	ACA	CTG	GTG	TGT	CTC	ATA	AGT	GAC	480
Glu	Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp	
145				150					155						160	
TTC	TAC	CCG	GGA	GCC	GTG	ACA	GTG	GCC	TGG	AAG	GCA	GAT	AGC	AGC	CCC	528
Phe	Tyr	Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	Ala	Asp	Ser	Ser	Pro	
			165					170					175			
GTC	AAG	GCG	GGA	GTG	GAG	ACC	ACC	ACA	CCC	TCC	AAA	CAA	AGC	AAC	AAC	576
Val	Lys	Ala	Gly	Val	Glu	Thr	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	Asn	

180								185				190				
AAG	TAC	GCG	GCC	AGC	AGC	TAC	CTG	AGC	CTG	ACG	CCT	GAG	CAG	TGG	AAG	624
Lys	Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys	
		195					200					205				
TCC	CAC	AGA	AGC	TAC	AGC	TGC	CAG	GTC	ACG	CAT	GAA	GGG	AGC	ACC	GTG	672
Ser	His	Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val	
	210					215					220					
GAG	AAG	ACA	GTG	GCC	CCT	ACA	GAA	TGT	TCA	TGA						705
Glu	Lys	Thr	Val	Ala	Pro	Thr	Glu	Cys	Ser	*						
225					230					235						

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Val	Pro	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Pro	
1				5				10						15		
Gly	Ala	Arg	Cys	Ala	Tyr	Glu	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Val	
			20					25					30			
Ser	Pro	Gly	Gln	Thr	Ala	Arg	Ile	Thr	Cys	Gly	Gly	Asp	Asn	Ser	Arg	
		35					40					45				
Asn	Glu	Tyr	Val	His	Trp	Tyr	Gln	Gln	Lys	Pro	Ala	Arg	Ala	Pro	Ile	
	50					55					60					
Leu	Val	Ile	Tyr	Asp	Asp	Ser	Asp	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	
65					70					75					80	
Phe	Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Asn	Gly	
				85					90					95		
Val	Glu	Ala	Gly	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Arg	
			100					105					110			
Ala	Ser	Asp	His	Pro	Val	Phe	Gly	Gly	Gly	Thr	Arg	Val	Thr	Val	Leu	
		115					120					125				
Gly	Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	
		130				135					140					
Glu	Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp	
145					150					155					160	

(2) INFORMATION FOR SEQ ID NO:3:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ix) **FEATURE:**

- (A) NAME/KEY: CDS
(B) LOCATION: 1..1431

(ix) **FEATURE:**

- ```
(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..1431
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AAT | CCC | TCC | CTC | AAG | AGT | CGA | GTC | ACC | ATT | TCA | AAA | GAC | ACG | TCC | AAG | 288 |
| Asn | Pro | Ser | Leu | Lys | Ser | Arg | Val | Thr | Ile | Ser | Lys | Asp | Thr | Ser | Lys |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| AAC | CAG | TTC | TTC | CTG | AAC | TTG | AAT | TCT | GTG | ACC | GAC | GCG | GAC | ACG | GCC | 336 |
| Asn | Gln | Phe | Phe | Leu | Asn | Leu | Asn | Ser | Val | Thr | Asp | Ala | Asp | Thr | Ala |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| GTC | TAT | TAC | TGT | GCG | AGA | GGC | CCT | CGC | CCT | GAT | TGC | ACA | ACC | ATT | TGT | 384 |
| Val | Tyr | Tyr | Cys | Ala | Arg | Gly | Pro | Arg | Pro | Asp | Cys | Thr | Thr | Ile | Cys |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| TAT | GGC | GGC | TGG | GTC | GAT | GTC | TGG | GGC | CCG | GGA | GAC | CTG | GTC | ACC | GTC | 432 |
| Tyr | Gly | Gly | Trp | Val | Asp | Val | Trp | Gly | Pro | Gly | Asp | Leu | Val | Thr | Val |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| TCC | TCA | GCT | AGC | ACC | AAG | GGC | CCA | TCG | GTC | TTC | CCC | CTG | GCA | CCC | TCC | 480 |
| Ser | Ser | Ala | Ser | Thr | Lys | Gly | Pro | Ser | Val | Phe | Pro | Leu | Ala | Pro | Ser |     |
|     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| TCC | AAG | AGC | ACC | TCT | GGG | GGC | ACA | GCG | GCC | CTG | GGC | TGC | CTG | GTC | AAG | 528 |
| Ser | Lys | Ser | Thr | Ser | Gly | Gly | Thr | Ala | Ala | Leu | Gly | Cys | Leu | Val | Lys |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| GAC | TAC | TTC | CCC | GAA | CCG | GTG | ACG | GTG | TCG | TGG | AAC | TCA | GGC | GCC | CTG | 576 |
| Asp | Tyr | Phe | Pro | Glu | Pro | Val | Thr | Val | Ser | Trp | Asn | Ser | Gly | Ala | Leu |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| ACC | AGC | GGC | GTG | CAC | ACC | TTC | CCG | GCT | GTC | CTA | CAG | TCC | TCA | GGA | CTC | 624 |
| Thr | Ser | Gly | Val | His | Thr | Phe | Pro | Ala | Val | Leu | Gln | Ser | Ser | Gly | Leu |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| TAC | TCC | CTC | AGC | AGC | GTG | GTG | ACC | GTG | CCC | TCC | AGC | AGC | TTG | GGC | ACC | 672 |
| Tyr | Ser | Leu | Ser | Ser | Val | Val | Thr | Val | Pro | Ser | Ser | Ser | Leu | Gly | Thr |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| CAG | ACC | TAC | ATC | TGC | AAC | GTG | AAT | CAC | AAG | CCC | AGC | AAC | ACC | AAG | GTG | 720 |
| Gln | Thr | Tyr | Ile | Cys | Asn | Val | Asn | His | Lys | Pro | Ser | Asn | Thr | Lys | Val |     |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| GAC | AAG | AAA | GCA | GAG | CCC | AAA | TCT | TGT | GAC | AAA | ACT | CAC | ACA | TGC | CCA | 768 |
| Asp | Lys | Lys | Ala | Glu | Pro | Lys | Ser | Cys | Asp | Lys | Thr | His | Thr | Cys | Pro |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| CCG | TGC | CCA | GCA | CCT | GAA | CTC | CTG | GGG | GGA | CCG | TCA | GTC | TTC | CTC | TTC | 816 |
| Pro | Cys | Pro | Ala | Pro | Glu | Leu | Leu | Gly | Gly | Pro | Ser | Val | Phe | Leu | Phe |     |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |     |
| CCC | CCA | AAA | CCC | AAG | GAC | ACC | CTC | ATG | ATC | TCC | CGG | ACC | CCT | GAG | GTC | 864 |
| Pro | Pro | Lys | Pro | Lys | Asp | Thr | Leu | Met | Ile | Ser | Arg | Thr | Pro | Glu | Val |     |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |
| ACA | TGC | GTG | GTG | GTG | GAC | GTG | AGC | CAC | GAA | GAC | CCT | GAG | GTC | AAG | TTC | 912 |
| Thr | Cys | Val | Val | Val | Asp | Val | Ser | His | Glu | Asp | Pro | Glu | Val | Lys | Phe |     |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |     |

AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG 960  
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
305 310 315 320  
CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC GTC CTC ACC 1008  
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr  
325 330 335  
GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC 1056  
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
340 345 350  
TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC 1104  
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala  
355 360 365  
AAA GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG 1152  
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
370 375 380  
GAT GAG CTG ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC 1200  
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
385 390 395 400  
TTC TAT CCC AGC GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG 1248  
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
405 410 415  
GAG AAC AAC TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC 1296  
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser  
420 425 430  
TTC TTC CTC TAC AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG 1344  
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
435 440 445  
GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC 1392  
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
450 455 460  
TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA 1431  
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys \*  
465 470 475

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

65

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 1 5 10 15  
 Val Leu Ser Gln Val Lys Leu Gln Gln Trp Gly Glu Gly Leu Leu Gln  
 20 25 30  
 Pro Ser Glu Thr Leu Ser Arg Thr Cys Val Val Ser Gly Gly Ser Ile  
 35 40 45  
 Ser Gly Tyr Tyr Tyr Trp Thr Trp Ile Arg Gln Thr Pro Gly Arg Gly  
 50 55 60  
 Leu Glu Trp Ile Gly His Ile Tyr Gly Asn Gly Ala Thr Thr Asn Tyr  
 65 70 75 80  
 Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Thr Ser Lys  
 85 90 95  
 Asn Gln Phe Phe Leu Asn Leu Asn Ser Val Thr Asp Ala Asp Thr Ala  
 100 105 110  
 Val Tyr Tyr Cys Ala Arg Gly Pro Arg Pro Asp Cys Thr Thr Ile Cys  
 115 120 125  
 Tyr Gly Gly Trp Val Asp Val Trp Gly Pro Gly Asp Leu Val Thr Val  
 130 135 140  
 Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
 145 150 155 160  
 Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
 165 170 175  
 Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
 180 185 190  
 Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
 195 200 205  
 Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
 210 215 220  
 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
 225 230 235 240  
 Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro  
 245 250 255  
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe  
 260 265 270  
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
 275 280 285  
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe  
 290 295 300

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro  
 305 310 315 320  
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr  
 325 330 335  
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
 340 345 350  
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala  
 355 360 365  
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
 370 375 380  
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
 385 390 395 400  
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
 405 410 415  
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser  
 420 425 430  
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
 435 440 445  
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
 450 455 460  
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys \*  
 465 470 475

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..720

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..720

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG AGC CTC CCT GCT CAG CTC CTC GGG CTG CTA TTG CTC TGC GTC CCC

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|                   |                   |                   |                   |                  |                   |                   |                   |                   |                   |                   |                   |                   |                   |                  |                   |  |     |
|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|--|-----|
| Met<br>1          | Ser               | Leu               | Pro               | Ala<br>5         | Gln               | Leu               | Leu               | Gly               | Leu<br>10         | Leu               | Leu               | Leu               | Cys               | Val<br>15        | Pro               |  |     |
| GGG<br>Gly        | TCC<br>Ser        | AGT<br>Ser        | GGG<br>Gly<br>20  | GAA<br>Glu       | GTT<br>Val        | GTG<br>Val        | ATG<br>Met        | ACT<br>Thr<br>25  | CAG<br>Gln        | TCT<br>Ser        | CCA<br>Pro        | CTG<br>Leu        | TCC<br>Ser<br>30  | CTT<br>Leu       | CCC<br>Pro        |  | 96  |
| ATC<br>Ile        | ACA<br>Thr        | CCT<br>Pro<br>35  | GGA<br>Gly        | GAG<br>Glu       | CCG<br>Pro        | GCC<br>Ala        | TCC<br>Ser<br>40  | ATC<br>Ile        | TCC<br>Ser        | TGT<br>Cys        | AGG<br>Arg        | TCT<br>Ser<br>45  | AGT<br>Ser        | CAA<br>Gln       | AGC<br>Ser        |  | 144 |
| CTT<br>Leu        | AAA<br>Lys<br>50  | CAC<br>His        | AGT<br>Ser        | AAT<br>Asn       | GGA<br>Gly        | GAC<br>Asp<br>55  | ACC<br>Thr        | TTC<br>Phe        | CTG<br>Leu        | AGT<br>Ser        | TGG<br>Trp<br>60  | TAT<br>Tyr        | CAG<br>Gln        | CAG<br>Gln       | AAG<br>Lys        |  | 192 |
| CCA<br>Pro<br>65  | GGC<br>Gly        | CAA<br>Gln        | CCT<br>Pro        | CCA<br>Pro       | AGG<br>Arg<br>70  | CTC<br>Leu        | CTG<br>Leu        | ATT<br>Ile        | TAT<br>Tyr        | AAG<br>Lys<br>75  | GTT<br>Val        | TCT<br>Ser        | AAC<br>Asn        | CGG<br>Arg       | GAC<br>Asp<br>80  |  | 240 |
| TCT<br>Ser        | GGG<br>Gly        | GTC<br>Val        | CCA<br>Pro        | GAC<br>Asp<br>85 | AGA<br>Arg        | TTC<br>Phe        | AGC<br>Ser        | GGC<br>Gly<br>90  | AGT<br>Ser        | GGG<br>Gly        | GCA<br>Ala        | GGG<br>Gly        | ACA<br>Thr        | GAT<br>Asp<br>95 | TTC<br>Phe        |  | 288 |
| ACA<br>Thr        | CTG<br>Leu        | AAA<br>Lys        | ATC<br>Ile<br>100 | AGC<br>Ser       | GCA<br>Ala        | GTG<br>Val        | GAG<br>Glu<br>105 | GCT<br>Ala        | GAA<br>Glu        | GAT<br>Asp        | GTT<br>Val        | GGG<br>Gly<br>110 | GTT<br>Val        | TAT<br>Tyr       | TTC<br>Phe        |  | 336 |
| TGC<br>Cys        | GGG<br>Gly        | CAA<br>Gln<br>115 | GGT<br>Gly        | ACA<br>Thr       | AGG<br>Arg        | ACT<br>Thr        | CCT<br>Pro<br>120 | CCC<br>Pro        | ACT<br>Thr        | TTC<br>Phe        | GGC<br>Gly        | GGA<br>Gly<br>125 | GGG<br>Gly        | ACC<br>Thr       | AAG<br>Lys        |  | 384 |
| GTG<br>Val<br>130 | GAA<br>Glu        | ATC<br>Ile        | AAA<br>Lys        | CGT<br>Arg       | ACG<br>Thr        | GTG<br>Val<br>135 | GCT<br>Ala        | GCA<br>Ala        | CCA<br>Pro        | TCT<br>Ser        | GTC<br>Val<br>140 | TTC<br>Phe        | ATC<br>Ile        | TTC<br>Phe       | CCG<br>Pro        |  | 432 |
| CCA<br>Pro<br>145 | TCT<br>Ser        | GAT<br>Asp        | GAG<br>Glu        | CAG<br>Gln       | TTG<br>Leu<br>150 | AAA<br>Lys        | TCT<br>Ser        | GGA<br>Gly        | ACT<br>Thr        | GCC<br>Ala<br>155 | TCT<br>Ser        | GTT<br>Val        | GTG<br>Val        | TGC<br>Cys       | CTG<br>Leu<br>160 |  | 480 |
| CTG<br>Leu        | AAT<br>Asn        | AAC<br>Asn        | TTC<br>Phe<br>165 | TAT<br>Tyr       | CCC<br>Pro        | AGA<br>Arg        | GAG<br>Glu        | GCC<br>Ala        | AAA<br>Lys<br>170 | GTA<br>Val        | CAG<br>Gln        | TGG<br>Trp        | AAG<br>Lys<br>175 | GTG<br>Val       | GAT<br>Asp        |  | 528 |
| AAC<br>Asn        | GCC<br>Ala        | CTC<br>Leu        | CAA<br>Gln<br>180 | TCG<br>Ser       | GGT<br>Gly        | AAC<br>Asn        | TCC<br>Ser        | CAG<br>Gln<br>185 | GAG<br>Glu        | AGT<br>Ser        | GTC<br>Val        | ACA<br>Thr        | GAG<br>Glu<br>190 | CAG<br>Gln       | GAC<br>Asp        |  | 576 |
| AGC<br>Ser        | AAG<br>Lys<br>195 | GAC<br>Asp        | AGC<br>Ser        | ACC<br>Thr       | TAC<br>Tyr        | AGC<br>Ser        | CTC<br>Leu<br>200 | AGC<br>Ser        | AGC<br>Ser        | ACC<br>Thr        | CTG<br>Leu        | ACG<br>Thr<br>205 | CTG<br>Leu        | AGC<br>Ser       | AAA<br>Lys        |  | 624 |
| GCA<br>Ala<br>210 | GAC<br>Asp        | TAC<br>Tyr        | GAG<br>Glu        | AAA<br>Lys       | CAC<br>His        | AAA<br>Lys<br>215 | GTC<br>Val        | TAC<br>Tyr        | GCC<br>Ala        | TGC<br>Cys        | GAA<br>Glu<br>220 | GTC<br>Val        | ACC<br>Thr        | CAT<br>His       | CAG<br>Gln        |  | 672 |
| GGC               | CTG               | AGC               | TCG               | CCC              | GTC               | ACA               | AAG               | AGC               | TTC               | AAC               | AGG               | GGA               | GAG               | TGT              | TGA               |  | 720 |

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys \*  
 225 230 235 240

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 240 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ser Leu Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Cys Val Pro  
 1 5 10 15  
 Gly Ser Ser Gly Glu Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro  
 20 25 30  
 Ile Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser  
 35 40 45  
 Leu Lys His Ser Asn Gly Asp Thr Phe Leu Ser Trp Tyr Gln Gln Lys  
 50 55 60  
 Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Asp  
 65 70 75 80  
 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe  
 85 90 95  
 Thr Leu Lys Ile Ser Ala Val Glu Ala Glu Asp Val Gly Val Tyr Phe  
 100 105 110  
 Cys Gly Gln Gly Thr Arg Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys  
 115 120 125  
 Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro  
 130 135 140  
 Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu  
 145 150 155 160  
 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp  
 165 170 175  
 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp  
 180 185 190  
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys  
 195 200 205  
 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln  
 210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys \*  
 225 230 235 240

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1437

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..1437

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | GGT | TGG | AGC | CTC | ATC | TTG | CTC | TTC | CTT | GTC | GCT | GTT | GCT | ACG | CGT | 48  |
| Met | Gly | Trp | Ser | Leu | Ile | Leu | Leu | Phe | Leu | Val | Ala | Val | Ala | Thr | Arg |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| GTC | CAG | TGT | GAG | GTG | CAA | CTG | GTG | GAG | TCT | GGG | GGA | GGC | TTG | GTC | CAG | 96  |
| Val | Gln | Cys | Glu | Val | Gln | Leu | Val | Glu | Ser | Gly | Gly | Gly | Leu | Val | Gln |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| CCT | GGC | GGG | TCC | CTG | AGA | GTC | TCC | TGT | GCA | GTC | TCT | GGA | TTC | ACC | TTC | 144 |
| Pro | Gly | Gly | Ser | Leu | Arg | Val | Ser | Cys | Ala | Val | Ser | Gly | Phe | Thr | Phe |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| AGT | GAC | CAC | TAC | ATG | TAT | TGG | TTC | CGC | CAG | GCT | CCA | GGG | AAG | GGG | CCG | 192 |
| Ser | Asp | His | Tyr | Met | Tyr | Trp | Phe | Arg | Gln | Ala | Pro | Gly | Lys | Gly | Pro |     |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| GAA | TGG | GTA | GGT | TTC | ATT | AGA | AAC | AAA | CCG | AAC | GGT | GGG | ACA | ACA | GAA | 240 |
| Glu | Trp | Val | Gly | Phe | Ile | Arg | Asn | Lys | Pro | Asn | Gly | Gly | Thr | Thr | Glu |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| TAC | GCC | GCG | TCT | GTG | AAA | GAC | AGA | TTC | ACC | ATC | TCC | AGA | GAT | GAT | TCC | 288 |
| Tyr | Ala | Ala | Ser | Val | Lys | Asp | Arg | Phe | Thr | Ile | Ser | Arg | Asp | Asp | Ser |     |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     | 95  |     |     |     |
| AAA | AGC | ATC | GCC | TAT | CTG | CAA | ATG | AGC | AGC | CTG | AAA | ATC | GAG | GAC | ACG | 336 |
| Lys | Ser | Ile | Ala | Tyr | Leu | Gln | Met | Ser | Ser | Leu | Lys | Ile | Glu | Asp | Thr |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| GCC | GTC | TAT | TAC | TGT | ACT | ACA | TCC | TAC | ATT | TCA | CAT | TGT | CGG | GGT | GGT | 384 |
| Ala | Val | Tyr | Tyr | Cys | Thr | Thr | Ser | Tyr | Ile | Ser | His | Cys | Arg | Gly | Gly |     |

| 115 |     |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |  |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|------|
| GTC | TGC | TAT | GGA | GGT | TAC | TTC | GAA | TTC | TGG | GGC | CAG | GGC | GCC | CTG | GTC |  |  | 432  |
| Val | Cys | Tyr | Gly | Gly | Tyr | Phe | Glu | Phe | Trp | Gly | Gln | Gly | Ala | Leu | Val |  |  |      |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |      |
| ACC | GTC | TCC | TCA | GCT | AGC | ACC | AAG | GGC | CCA | TCG | GTC | TTC | CCC | CTG | GCA |  |  | 480  |
| Thr | Val | Ser | Ser | Ala | Ser | Thr | Lys | Gly | Pro | Ser | Val | Phe | Pro | Leu | Ala |  |  |      |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |      |
| CCC | TCC | TCC | AAG | AGC | ACC | TCT | GGG | GGC | ACA | GCG | GCC | CTG | GGC | TGC | CTG |  |  | 528  |
| Pro | Ser | Ser | Lys | Ser | Thr | Ser | Gly | Gly | Thr | Ala | Ala | Leu | Gly | Cys | Leu |  |  |      |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |      |
| GTC | AAG | GAC | TAC | TTC | CCC | GAA | CCG | GTG | ACG | GTG | TCG | TGG | AAC | TCA | GGC |  |  | 576  |
| Val | Lys | Asp | Tyr | Phe | Pro | Glu | Pro | Val | Thr | Val | Ser | Trp | Asn | Ser | Gly |  |  |      |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |      |
| GCC | CTG | ACC | AGC | GGC | GTG | CAC | ACC | TTC | CCG | GCT | GTC | CTA | CAG | TCC | TCA |  |  | 624  |
| Ala | Leu | Thr | Ser | Gly | Val | His | Thr | Phe | Pro | Ala | Val | Leu | Gln | Ser | Ser |  |  |      |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |      |
| GGA | CTC | TAC | TCC | CTC | AGC | AGC | GTG | GTG | ACC | GTG | CCC | TCC | AGC | AGC | TTG |  |  | 672  |
| Gly | Leu | Tyr | Ser | Leu | Ser | Ser | Val | Val | Thr | Val | Pro | Ser | Ser | Ser | Leu |  |  |      |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |      |
| GGC | ACC | CAG | ACC | TAC | ATC | TGC | AAC | GTG | AAT | CAC | AAG | CCC | AGC | AAC | ACC |  |  | 720  |
| Gly | Thr | Gln | Thr | Tyr | Ile | Cys | Asn | Val | Asn | His | Lys | Pro | Ser | Asn | Thr |  |  |      |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |      |
| AAG | GTG | GAC | AAG | AAA | GCA | GAG | CCC | AAA | TCT | TGT | GAC | AAA | ACT | CAC | ACA |  |  | 768  |
| Lys | Val | Asp | Lys | Lys | Ala | Glu | Pro | Lys | Ser | Cys | Asp | Lys | Thr | His | Thr |  |  |      |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |      |
| TGC | CCA | CCG | TGC | CCA | GCA | CCT | GAA | CTC | CTG | GGG | GGA | CCG | TCA | GTC | TTC |  |  | 816  |
| Cys | Pro | Pro | Cys | Pro | Ala | Pro | Glu | Leu | Leu | Gly | Gly | Pro | Ser | Val | Phe |  |  |      |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |      |
| CTC | TTC | CCC | CCA | AAA | CCC | AAG | GAC | ACC | CTC | ATG | ATC | TCC | CGG | ACC | CCT |  |  | 864  |
| Leu | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Thr | Leu | Met | Ile | Ser | Arg | Thr | Pro |  |  |      |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |      |
| GAG | GTC | ACA | TGC | GTG | GTG | GTG | GAC | GTG | AGC | CAC | GAA | GAC | CCT | GAG | GTC |  |  | 912  |
| Glu | Val | Thr | Cys | Val | Val | Val | Asp | Val | Ser | His | Glu | Asp | Pro | Glu | Val |  |  |      |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |      |
| AAG | TTC | AAC | TGG | TAC | GTG | GAC | GGC | GTG | GAG | GTG | CAT | AAT | GCC | AAG | ACA |  |  | 960  |
| Lys | Phe | Asn | Trp | Tyr | Val | Asp | Gly | Val | Glu | Val | His | Asn | Ala | Lys | Thr |  |  |      |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |  |      |
| AAG | CCG | CGG | GAG | GAG | CAG | TAC | AAC | AGC | ACG | TAC | CGT | GTG | GTC | AGC | GTC |  |  | 1008 |
| Lys | Pro | Arg | Glu | Glu | Gln | Tyr | Asn | Ser | Thr | Tyr | Arg | Val | Val | Ser | Val |  |  |      |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |  |      |
| CTC | ACC | GTC | CTG | CAC | CAG | GAC | TGG | CTG | AAT | GGC | AAG | GAG | TAC | AAG | TGC |  |  | 1056 |
| Leu | Thr | Val | Leu | His | Gln | Asp | Trp | Leu | Asn | Gly | Lys | Glu | Tyr | Lys | Cys |  |  |      |

| 340 |     |     |     |     |     |     |     |     |     | 345 |     |     |     |     | 350 |  |  |  |  |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|------|
| AAG | GTC | TCC | AAC | AAA | GCC | CTC | CCA | GCC | CCC | ATC | GAG | AAA | ACC | ATC | TCC |  |  |  |  | 1104 |
| Lys | Val | Ser | Asn | Lys | Ala | Leu | Pro | Ala | Pro | Ile | Glu | Lys | Thr | Ile | Ser |  |  |  |  |      |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |  |  |  |      |
| AAA | GCC | AAA | GGG | CAG | CCC | CGA | GAA | CCA | CAG | GTG | TAC | ACC | CTG | CCC | CCA |  |  |  |  | 1152 |
| Lys | Ala | Lys | Gly | Gln | Pro | Arg | Glu | Pro | Gln | Val | Tyr | Thr | Leu | Pro | Pro |  |  |  |  |      |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |  |  |  |  |      |
| TCC | CGG | GAT | GAG | CTG | ACC | AAG | AAC | CAG | GTC | AGC | CTG | ACC | TGC | CTG | GTC |  |  |  |  | 1200 |
| Ser | Arg | Asp | Glu | Leu | Thr | Lys | Asn | Gln | Val | Ser | Leu | Thr | Cys | Leu | Val |  |  |  |  |      |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |  |  |  |  |      |
| AAA | GGC | TTC | TAT | CCC | AGC | GAC | ATC | GCC | GTG | GAG | TGG | GAG | AGC | AAT | GGG |  |  |  |  | 1248 |
| Lys | Gly | Phe | Tyr | Pro | Ser | Asp | Ile | Ala | Val | Glu | Trp | Glu | Ser | Asn | Gly |  |  |  |  |      |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |  |  |  |  |      |
| CAG | CCG | GAG | AAC | AAC | TAC | AAG | ACC | ACG | CCT | CCC | GTG | CTG | GAC | TCC | GAC |  |  |  |  | 1296 |
| Gln | Pro | Glu | Asn | Asn | Tyr | Lys | Thr | Thr | Pro | Pro | Val | Leu | Asp | Ser | Asp |  |  |  |  |      |
|     |     |     | 420 |     |     |     | 425 |     |     |     |     |     | 430 |     |     |  |  |  |  |      |
| GGC | TCC | TTC | TTC | CTC | TAC | AGC | AAG | CTC | ACC | GTG | GAC | AAG | AGC | AGG | TGG |  |  |  |  | 1344 |
| Gly | Ser | Phe | Phe | Leu | Tyr | Ser | Lys | Leu | Thr | Val | Asp | Lys | Ser | Arg | Trp |  |  |  |  |      |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |  |  |  |  |      |
| CAG | CAG | GGG | AAC | GTC | TTC | TCA | TGC | TCC | GTG | ATG | CAT | GAG | GCT | CTG | CAC |  |  |  |  | 1392 |
| Gln | Gln | Gly | Asn | Val | Phe | Ser | Cys | Ser | Val | Met | His | Glu | Ala | Leu | His |  |  |  |  |      |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |  |  |  |  |      |
| AAC | CAC | TAC | ACG | CAG | AAG | AGC | CTC | TCC | CTG | TCT | CCG | GGT | AAA | TGA |     |  |  |  |  | 1437 |
| Asn | His | Tyr | Thr | Gln | Lys | Ser | Leu | Ser | Leu | Ser | Pro | Gly | Lys | *   |     |  |  |  |  |      |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     |     |  |  |  |  |      |

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg  
 1 5 10 15

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln  
 20 25 30

Pro Gly Gly Ser Leu Arg Val Ser Cys Ala Val Ser Gly Phe Thr Phe  
 35 40 45

Ser Asp His Tyr Met Tyr Trp Phe Arg Gln Ala Pro Gly Lys Gly Pro

50

55

60

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Glu<br>65  | Trp        | Val        | Gly        | Phe        | Ile<br>70  | Arg        | Asn        | Lys        | Pro        | Asn<br>75  | Gly        | Gly        | Thr        | Thr        | Glu<br>80  |
| Tyr        | Ala        | Ala        | Ser        | Val<br>85  | Lys        | Asp        | Arg        | Phe        | Thr<br>90  | Ile        | Ser        | Arg        | Asp        | Asp        | Ser        |
| Lys        | Ser        | Ile        | Ala<br>100 | Tyr        | Leu        | Gln        | Met        | Ser        | Ser        | Leu        | Lys        | Ile        | Glu<br>110 | Asp        | Thr        |
| Ala        | Val        | Tyr<br>115 | Tyr        | Cys        | Thr        | Thr        | Ser<br>120 | Tyr        | Ile        | Ser        | His        | Cys<br>125 | Arg        | Gly        | Gly        |
| Val        | Cys<br>130 | Tyr        | Gly        | Gly        | Tyr        | Phe<br>135 | Glu        | Phe        | Trp        | Gly        | Gln<br>140 | Gly        | Ala        | Leu        | Val        |
| Thr<br>145 | Val        | Ser        | Ser        | Ala        | Ser<br>150 | Thr        | Lys        | Gly        | Pro        | Ser<br>155 | Val        | Phe        | Pro        | Leu        | Ala<br>160 |
| Pro        | Ser        | Ser        | Lys        | Ser<br>165 | Thr        | Ser        | Gly        | Gly        | Thr<br>170 | Ala        | Ala        | Leu        | Gly        | Cys<br>175 | Leu        |
| Val        | Lys        | Asp        | Tyr<br>180 | Phe        | Pro        | Glu        | Pro<br>185 | Val        | Thr        | Val        | Ser        | Trp        | Asn<br>190 | Ser        | Gly        |
| Ala        | Leu        | Thr<br>195 | Ser        | Gly        | Val        | His        | Thr<br>200 | Phe        | Pro        | Ala        | Val        | Leu        | Gln        | Ser        | Ser        |
| Gly        | Leu<br>210 | Tyr        | Ser        | Leu        | Ser        | Ser        | Val<br>215 | Val        | Thr        | Val        | Pro        | Ser        | Ser        | Ser        | Leu        |
| Gly<br>225 | Thr        | Gln        | Thr        | Tyr        | Ile<br>230 | Cys        | Asn        | Val        | Asn        | His<br>235 | Lys        | Pro        | Ser        | Asn        | Thr<br>240 |
| Lys        | Val        | Asp        | Lys        | Lys<br>245 | Ala        | Glu        | Pro        | Lys        | Ser<br>250 | Cys        | Asp        | Lys        | Thr        | His<br>255 | Thr        |
| Cys        | Pro        | Pro        | Cys<br>260 | Pro        | Ala        | Pro        | Glu        | Leu<br>265 | Leu        | Gly        | Gly        | Pro        | Ser<br>270 | Val        | Phe        |
| Leu        | Phe<br>275 | Pro        | Pro        | Lys        | Pro        | Lys        | Asp<br>280 | Thr        | Leu        | Met        | Ile        | Ser<br>285 | Arg        | Thr        | Pro        |
| Glu<br>290 | Val        | Thr        | Cys        | Val        | Val<br>295 | Val        | Asp        | Val        | Ser        | His        | Glu<br>300 | Asp        | Pro        | Glu        | Val        |
| Lys<br>305 | Phe        | Asn        | Trp        | Tyr        | Val<br>310 | Asp        | Gly        | Val        | Glu        | Val<br>315 | His        | Asn        | Ala        | Lys        | Thr<br>320 |
| Lys        | Pro        | Arg        | Glu        | Glu<br>325 | Gln        | Tyr        | Asn        | Ser        | Thr<br>330 | Tyr        | Arg        | Val        | Val        | Ser<br>335 | Val        |
| Leu        | Thr        | Val        | Leu<br>340 | His        | Gln        | Asp        | Trp        | Leu<br>345 | Asn        | Gly        | Lys        | Glu        | Tyr<br>350 | Lys        | Cys        |

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
 355 360 365  
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
 370 375 380  
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val  
 385 390 395 400  
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly  
 405 410 415  
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp  
 420 425 430  
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp  
 435 440 445  
 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His  
 450 455 460  
 Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys \*  
 465 470 475

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..711

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..711

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | AGG | GTC | CCC | GCT | CAG | CTC | CTG | GGG | CTC | CTG | CTG | CTC | TGG | CTC | CCA | 48  |
| Met | Arg | Val | Pro | Ala | Gln | Leu | Leu | Gly | Leu | Leu | Leu | Leu | Trp | Leu | Pro |     |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |     |
| GGT | GCA | CGA | TGT | GAG | TCT | GTC | CTG | ACA | CAG | CCG | CCC | TCA | GTG | TCT | GGG | 96  |
| Gly | Ala | Arg | Cys | Glu | Ser | Val | Leu | Thr | Gln | Pro | Pro | Ser | Val | Ser | Gly |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| GCC | CCA | GGG | CAG | AAG | GTC | ACC | ATC | TCG | TGC | ACT | GGG | AGC | ACC | TCC | AAC | 144 |
| Ala | Pro | Gly | Gln | Lys | Val | Thr | Ile | Ser | Cys | Thr | Gly | Ser | Thr | Ser | Asn |     |

| 35                                                                                                                                                    | 40 | 45 |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|----|----|-----|
| ATT GGA GGT TAT GAT CTA CAT TGG TAC CAG CAG CTC CCA GGA ACG GCC<br>Ile Gly Gly Tyr Asp Leu His Trp Tyr Gln Gln Leu Pro Gly Thr Ala<br>50 55 60        |    |    | 192 |
| CCC AAA CTC CTC ATC TAT GAC ATT AAC AAG CGA CCC TCA GGA ATT TCT<br>Pro Lys Leu Leu Ile Tyr Asp Ile Asn Lys Arg Pro Ser Gly Ile Ser<br>65 70 75 80     |    |    | 240 |
| GAC CGA TTC TCT GGC TCC AAG TCT GGT ACC GCG GCC TCC CTG GCC ATC<br>Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ala Ala Ser Leu Ala Ile<br>85 90 95        |    |    | 288 |
| ACT GGG CTC CAG ACT GAG GAT GAG GCT GAT TAT TAC TGC CAG TCC TAT<br>Thr Gly Leu Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr<br>100 105 110     |    |    | 336 |
| GAC AGC AGC CTG AAT GCT CAG GTA TTC GGA GGA GGG ACC CGG CTG ACC<br>Asp Ser Ser Leu Asn Ala Gln Val Phe Gly Gly Gly Thr Arg Leu Thr<br>115 120 125     |    |    | 384 |
| GTC CTA GGT CAG CCC AAG GCT GCC CCC TCG GTC ACT CTG TTC CCG CCC<br>Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro<br>130 135 140     |    |    | 432 |
| TCC TCT GAG GAG CTT CAA GCC AAC AAG GCC ACA CTG GTG TGT CTC ATA<br>Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile<br>145 150 155 160 |    |    | 480 |
| AGT GAC TTC TAC CCG GGA GCC GTG ACA GTG GCC TGG AAG GCA GAT AGC<br>Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser<br>165 170 175     |    |    | 528 |
| AGC CCC GTC AAG GCG GGA GTG GAG ACC ACC ACA CCC TCC AAA CAA AGC<br>Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser<br>180 185 190     |    |    | 576 |
| AAC AAC AAG TAC GCG GCC AGC AGC TAC CTG AGC CTG ACG CCT GAG CAG<br>Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln<br>195 200 205     |    |    | 624 |
| TGG AAG TCC CAC AGA AGC TAC AGC TGC CAG GTC ACG CAT GAA GGG AGC<br>Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser<br>210 215 220     |    |    | 672 |
| ACC GTG GAG AAG ACA GTG GCC CCT ACA GAA TGT TCA TGA<br>Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser *<br>225 230 235                               |    |    | 711 |

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

75



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp Leu Pro  
 1 5 10 15  
 Gly Ala Arg Cys Glu Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly  
 20 25 30  
 Ala Pro Gly Gln Lys Val Thr Ile Ser Cys Thr Gly Ser Thr Ser Asn  
 35 40 45  
 Ile Gly Gly Tyr Asp Leu His Trp Tyr Gln Gln Leu Pro Gly Thr Ala  
 50 55 60  
 Pro Lys Leu Leu Ile Tyr Asp Ile Asn Lys Arg Pro Ser Gly Ile Ser  
 65 70 75 80  
 Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ala Ala Ser Leu Ala Ile  
 85 90 95  
 Thr Gly Leu Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr  
 100 105 110  
 Asp Ser Ser Leu Asn Ala Gln Val Phe Gly Gly Gly Thr Arg Leu Thr  
 115 120 125  
 Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro  
 130 135 140  
 Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile  
 145 150 155 160  
 Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser  
 165 170 175  
 Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser  
 180 185 190  
 Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln  
 195 200 205  
 Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser  
 210 215 220  
 Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser \*  
 225 230 235

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1431 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..1431

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 1..1431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | AAA | CAC | CTG | TGG | TTC | TTC | CTC | CTC | CTG | GTG | GCA | GCT | CCC | AGA | TGG | 48  |
| Met | Lys | His | Leu | Trp | Phe | Phe | Leu | Leu | Leu | Val | Ala | Ala | Pro | Arg | Trp |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| GTC | CTG | TCC | CAG | GTG | CAG | CTG | CAG | GAG | TCG | GGC | CCA | GGA | CTG | GTG | AAG | 96  |
| Val | Leu | Ser | Gln | Val | Gln | Leu | Gln | Glu | Ser | Gly | Pro | Gly | Leu | Val | Lys |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| CCT | TCG | GAG | ACC | CTG | TCC | CTC | ACC | TGC | GCT | GTC | TCT | GGT | GGC | TCC | ATC | 144 |
| Pro | Ser | Glu | Thr | Leu | Ser | Leu | Thr | Cys | Ala | Val | Ser | Gly | Gly | Ser | Ile |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| AGC | GGT | GGT | TAT | GGC | TGG | GGC | TGG | ATC | CGC | CAG | CCC | CCA | GGG | AAG | GGG | 192 |
| Ser | Gly | Gly | Tyr | Gly | Trp | Gly | Trp | Ile | Arg | Gln | Pro | Pro | Gly | Lys | Gly |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| CTG | GAG | TGG | ATT | GGG | AGT | TTC | TAT | AGT | AGT | AGT | GGG | AAC | ACC | TAC | TAC | 240 |
| Leu | Glu | Trp | Ile | Gly | Ser | Phe | Tyr | Ser | Ser | Ser | Gly | Asn | Thr | Tyr | Tyr |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |     |
| AAC | CCC | TCC | CTC | AAG | AGT | CAA | GTC | ACC | ATT | TCA | ACA | GAC | ACG | TCC | AAG | 288 |
| Asn | Pro | Ser | Leu | Lys | Ser | Gln | Val | Thr | Ile | Ser | Thr | Asp | Thr | Ser | Lys |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| AAC | CAG | TTC | TCC | CTG | AAG | CTG | AAC | TCT | ATG | ACC | GCC | GCG | GAC | ACG | GCC | 336 |
| Asn | Gln | Phe | Ser | Leu | Lys | Leu | Asn | Ser | Met | Thr | Ala | Ala | Asp | Thr | Ala |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| GTG | TAT | TAC | TGT | GTG | AGA | GAT | CGT | CTT | TTT | TCA | GTT | GTT | GGA | ATG | GTT | 384 |
| Val | Tyr | Tyr | Cys | Val | Arg | Asp | Arg | Leu | Phe | Ser | Val | Val | Gly | Met | Val |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| TAC | AAC | AAC | TGG | TTC | GAT | GTC | TGG | GGC | CCG | GGA | GTC | CTG | GTC | ACC | GTC | 432 |
| Tyr | Asn | Asn | Trp | Phe | Asp | Val | Trp | Gly | Pro | Gly | Val | Leu | Val | Thr | Val |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| TCC | TCA | GCT | AGC | ACC | AAG | GGC | CCA | TCG | GTC | TTC | CCC | CTG | GCA | CCC | TCC | 480 |
| Ser | Ser | Ala | Ser | Thr | Lys | Gly | Pro | Ser | Val | Phe | Pro | Leu | Ala | Pro | Ser |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| TCC | AAG | AGC | ACC | TCT | GGG | GGC | ACA | GCG | GCC | CTG | GGC | TGC | CTG | GTC | AAG | 528  |
| Ser | Lys | Ser | Thr | Ser | Gly | Gly | Thr | Ala | Ala | Leu | Gly | Cys | Leu | Val | Lys |      |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |      |
| GAC | TAC | TTC | CCC | GAA | CCG | GTG | ACG | GTG | TCG | TGG | AAC | TCA | GGC | GCC | CTG | 576  |
| Asp | Tyr | Phe | Pro | Glu | Pro | Val | Thr | Val | Ser | Trp | Asn | Ser | Gly | Ala | Leu |      |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |      |
| ACC | AGC | GGC | GTG | CAC | ACC | TTC | CCG | GCT | GTC | CTA | CAG | TCC | TCA | GGA | CTC | 624  |
| Thr | Ser | Gly | Val | His | Thr | Phe | Pro | Ala | Val | Leu | Gln | Ser | Ser | Gly | Leu |      |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |      |
| TAC | TCC | CTC | AGC | AGC | GTG | GTG | ACC | GTG | CCC | TCC | AGC | AGC | TTG | GGC | ACC | 672  |
| Tyr | Ser | Leu | Ser | Ser | Val | Val | Thr | Val | Pro | Ser | Ser | Ser | Leu | Gly | Thr |      |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |      |
| CAG | ACC | TAC | ATC | TGC | AAC | GTG | AAT | CAC | AAG | CCC | AGC | AAC | ACC | AAG | GTG | 720  |
| Gln | Thr | Tyr | Ile | Cys | Asn | Val | Asn | His | Lys | Pro | Ser | Asn | Thr | Lys | Val |      |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |      |
| GAC | AAG | AAA | GCA | GAG | CCC | AAA | TCT | TGT | GAC | AAA | ACT | CAC | ACA | TGC | CCA | 768  |
| Asp | Lys | Lys | Ala | Glu | Pro | Lys | Ser | Cys | Asp | Lys | Thr | His | Thr | Cys | Pro |      |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |      |
| CCG | TGC | CCA | GCA | CCT | GAA | CTC | CTG | GGG | GGA | CCG | TCA | GTC | TTC | CTC | TTC | 816  |
| Pro | Cys | Pro | Ala | Pro | Glu | Leu | Leu | Gly | Gly | Pro | Ser | Val | Phe | Leu | Phe |      |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |      |
| CCC | CCA | AAA | CCC | AAG | GAC | ACC | CTC | ATG | ATC | TCC | CGG | ACC | CCT | GAG | GTC | 864  |
| Pro | Pro | Lys | Pro | Lys | Asp | Thr | Leu | Met | Ile | Ser | Arg | Thr | Pro | Glu | Val |      |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |      |
| ACA | TGC | GTG | GTG | GTG | GAC | GTG | AGC | CAC | GAA | GAC | CCT | GAG | GTC | AAG | TTC | 912  |
| Thr | Cys | Val | Val | Val | Asp | Val | Ser | His | Glu | Asp | Pro | Glu | Val | Lys | Phe |      |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |      |
| AAC | TGG | TAC | GTG | GAC | GGC | GTG | GAG | GTG | CAT | AAT | GCC | AAG | ACA | AAG | CCG | 960  |
| Asn | Trp | Tyr | Val | Asp | Gly | Val | Glu | Val | His | Asn | Ala | Lys | Thr | Lys | Pro |      |
| 305 |     |     |     |     | 310 |     |     |     | 315 |     |     |     |     |     | 320 |      |
| CGG | GAG | GAG | CAG | TAC | AAC | AGC | ACG | TAC | CGT | GTG | GTC | AGC | GTC | CTC | ACC | 1008 |
| Arg | Glu | Glu | Gln | Tyr | Asn | Ser | Thr | Tyr | Arg | Val | Val | Ser | Val | Leu | Thr |      |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |      |
| GTC | CTG | CAC | CAG | GAC | TGG | CTG | AAT | GGC | AAG | GAG | TAC | AAG | TGC | AAG | GTC | 1056 |
| Val | Leu | His | Gln | Asp | Trp | Leu | Asn | Gly | Lys | Glu | Tyr | Lys | Cys | Lys | Val |      |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |      |
| TCC | AAC | AAA | GCC | CTC | CCA | GCC | CCC | ATC | GAG | AAA | ACC | ATC | TCC | AAA | GCC | 1104 |
| Ser | Asn | Lys | Ala | Leu | Pro | Ala | Pro | Ile | Glu | Lys | Thr | Ile | Ser | Lys | Ala |      |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |      |
| AAA | GGG | CAG | CCC | CGA | GAA | CCA | CAG | GTG | TAC | ACC | CTG | CCC | CCA | TCC | CGG | 1152 |
| Lys | Gly | Gln | Pro | Arg | Glu | Pro | Gln | Val | Tyr | Thr | Leu | Pro | Pro | Ser | Arg |      |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |      |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| GAT | GAG | CTG | ACC | AAG | AAC | CAG | GTC | AGC | CTG | ACC | TGC | CTG | GTC | AAA | GGC | 1200 |
| Asp | Glu | Leu | Thr | Lys | Asn | Gln | Val | Ser | Leu | Thr | Cys | Leu | Val | Lys | Gly |      |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |      |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
| TTC | TAT | CCC | AGC | GAC | ATC | GCC | GTG | GAG | TGG | GAG | AGC | AAT | GGG | CAG | CCG | 1248 |
| Phe | Tyr | Pro | Ser | Asp | Ile | Ala | Val | Glu | Trp | Glu | Ser | Asn | Gly | Gln | Pro |      |
|     |     |     |     | 405 |     |     |     | 410 |     |     |     |     |     | 415 |     |      |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
| GAG | AAC | AAC | TAC | AAG | ACC | ACG | CCT | CCC | GTG | CTG | GAC | TCC | GAC | GGC | TCC | 1296 |
| Glu | Asn | Asn | Tyr | Lys | Thr | Thr | Pro | Pro | Val | Leu | Asp | Ser | Asp | Gly | Ser |      |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |      |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
| TTC | TTC | CTC | TAC | AGC | AAG | CTC | ACC | GTG | GAC | AAG | AGC | AGG | TGG | CAG | CAG | 1344 |
| Phe | Phe | Leu | Tyr | Ser | Lys | Leu | Thr | Val | Asp | Lys | Ser | Arg | Trp | Gln | Gln |      |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |      |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
| GGG | AAC | GTC | TTC | TCA | TGC | TCC | GTG | ATG | CAT | GAG | GCT | CTG | CAC | AAC | CAC | 1392 |
| Gly | Asn | Val | Phe | Ser | Cys | Ser | Val | Met | His | Glu | Ala | Leu | His | Asn | His |      |
| 450 |     |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |      |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
| TAC | ACG | CAG | AAG | AGC | CTC | TCC | CTG | TCT | CCG | GGT | AAA | TGA |     |     |     | 1431 |
| Tyr | Thr | Gln | Lys | Ser | Leu | Ser | Leu | Ser | Pro | Gly | Lys | *   |     |     |     |      |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     |     |      |

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | His | Leu | Trp | Phe | Phe | Leu | Leu | Leu | Val | Ala | Ala | Pro | Arg | Trp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Val | Leu | Ser | Gln | Val | Gln | Leu | Gln | Glu | Ser | Gly | Pro | Gly | Leu | Val | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Pro | Ser | Glu | Thr | Leu | Ser | Leu | Thr | Cys | Ala | Val | Ser | Gly | Gly | Ser | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ser | Gly | Gly | Tyr | Gly | Trp | Gly | Trp | Ile | Arg | Gln | Pro | Pro | Gly | Lys | Gly |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Leu | Glu | Trp | Ile | Gly | Ser | Phe | Tyr | Ser | Ser | Ser | Gly | Asn | Thr | Tyr | Tyr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Asn | Pro | Ser | Leu | Lys | Ser | Gln | Val | Thr | Ile | Ser | Thr | Asp | Thr | Ser | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Asn | Gln | Phe | Ser | Leu | Lys | Leu | Asn | Ser | Met | Thr | Ala | Ala | Asp | Thr | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

20

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser  
 420 425 430

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
 435 440 445

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
 450 455 460

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys \*  
 465 470 475

09333916 082699